AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please replace the paragraphs spanning lines 4-23 of page 12 with the following replacement paragraph:

Thus, plant zinc finger proteins are characterized by long spacers of diverse lengths between adjacent fingers. Moreover, they are characterised by a highly conserved sequence of six amino acids, located within a putative DNA-contacting surface of each finger. Two forms of such conserved sequence are most commonly found in plant C2H2 zinc fingers, the QALGGH (SEQ ID NO 5) and the NNM/WQMH (SEQ ID NO 6). Despite the high sequence conservation of the QALGGH (SEQ ID NO:5), some variants or the so-called 'modified type' occur in nature where one or two amino acids can have a different form, most typically the +1 "Q" can be a "G"," K" or "R" (these amino acids share the same turn-like characteristic), the +2 "A" can be "S" (both of which share the characteristic of being small amino acids) or the +3" "L can be "F" (these two amino acids are both hydrophobic). The QALGGH-motif (SEQ ID NO:5) as used herein comprises all these variants. In the NNM/WQMH (SEQ ID NO:6) motif at position 3 there is mostly an "M" or a "W".

Therefore, the present invention provides a method as described hereinabove, wherein said 2xC2H2 zinc finger protein comprises a QALGGH (SEQ ID NO:5) motif. Further, The present invention provides as described hereinabove, wherein said 2xC2H2 zinc finger protein comprises a NNM/WQMH (SEQ ID NO:6) motif.

According to one embodiment of the invention, both C2H2 domains are of the same type. More preferably, both C2H2 zinc finger domains have the same conserved QALGGH (SEQ ID NO:5) [[GALGGH]] or NNM/WQMH (SEQ ID NO:6) motif. According to another embodiment, each C2H2 zinc finger domain has a different conserved motif.

Please replace the paragraph spanning lines 11-20 of page 17 with the following replacement paragraph:

"Insertional variants" of a protein are those in which one or more amino acid residues are introduced into a predetermined site in said protein. Insertions can comprise amino-terminal and/or carboxy-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions, of the order of about 1 to 10 residues. Examples of amino- or carboxy-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, $(histidine)_6$(SEQ ID NO:52)-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag•100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

Please replace the paragraph spanning lines 27-37 of page 34 with the following replacement paragraph:

Fig. 3 lists sequences useful in the methods of the present invention. SEQ ID NO: 1 is an STZ encoding nucleic acid isolated from *Arabidopsis thaliana*; the start and the stop codon are highlighted in bold. SEQ ID NO: 2 is the STZ protein sequence encoded by SEQ ID NO: 1. In the STZ protein the nuclear localization signal also called the KRS motif or B-box is annotated (bold, italics, underlined), as well as the L-box (bold, underlined), the EAR motif (bold, italics), and the two C2H2 zinc finger domains with QALGGH (SEQ ID NO:5) motif (bold and boxed). SEQ ID NO: 10 to SEQ ID NO: 25 provides the sequences of various orthologs of the *Arabidopsis thaliana* STZ protein from other plant species. SEQ ID NO: 26 to SEQ ID NO: 35 provides the sequences of various paralogs (from *Arabidopsis*) of the STZ protein. SEQ ID NO: 36 to SEQ ID NO: 50 provides the sequences of related 2xC2H2 genes and proteins useful in the methods of the present invention.

Please insert the attached Sequence Listing in place of the Sequence Listing filed June 7, 2005.